

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (I) APPLICANT: DUAN, D. ROXANNE
SHILATIFARD, ALI
CONAWAY, JOAN W.
CONAWAY, RONALD C.
- (ii) TITLE OF INVENTION: ELL2, A New Member of an ELL Family of
RNA Polymerase II Elongation Factors
- (iii) NUMBER OF SEQUENCES: 34
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
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(C) CITY: WASHINGTON
(D) STATE: D.C.
(E) COUNTRY: USA
(F) ZIP: 20005-3934
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: To be assigned
(B) FILING DATE: Herewith
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/038,447
(B) FILING DATE: 19-FEB-1997
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: GOLDSTEIN, JORGE A.
(B) REGISTRATION NUMBER: 29,021
(C) REFERENCE/DOCKET NUMBER: 1488.0880001
- (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2139 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 94..2013

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAGTGGCGGC GGGTGCAGAA GCCCAAGCAG CGCGGCCGCA GTGGAGGCTA GAGCCGGAGC	60
GGCGGCGGCG GCGGCACCCC GGGGAGGTTT AAG ATG GCG GCG GGG GGG ACA GGG	114
Met Ala Ala Gly Gly Thr Gly	
1 5	
GGC CTG CGG GAG GAG CAG CGC TAT GGG CTG TCG TGC GGA CGG CTG GGG	162
Gly Leu Arg Glu Glu Gln Arg Tyr Gly Leu Ser Cys Gly Arg Leu Gly	
10 15 20	
CAG GAC AAC ATC ACC GTA CTG CAT GTG AAG CTC ACC GAG ACG GCG ATC	210
Gln Asp Asn Ile Thr Val Leu His Val Lys Leu Thr Glu Thr Ala Ile	
25 30 35	
CGG GCG CTC GAG ACT TAC CAG AGC CAC AAG AAT TTA ATT CCT TTT CGA	258
Arg Ala Leu Glu Thr Tyr Gln Ser His Lys Asn Leu Ile Pro Phe Arg	
40 45 50 55	
CCT TCA ATC CAG TTC CAA GGA CTC CAC GGG CTT GTC AAA ATT CCC AAA	306
Pro Ser Ile Gln Phe Gln Gly Leu His Gly Leu Val Lys Ile Pro Lys	
60 65 70	
AAT GAT CCC CTC AAT GAA GTT CAT AAC TTT AAC TTT TAT TTG TCA AAT	354
Asn Asp Pro Leu Asn Glu Val His Asn Phe Asn Phe Tyr Leu Ser Asn	
75 80 85	
GTG GGC AAA GAC AAC CCT CAG GGC AGC TTT GAC TGC ATC CAG CAA ACA	402
Val Gly Lys Asp Asn Pro Gln Gly Ser Phe Asp Cys Ile Gln Gln Thr	
90 95 100	
TTC TCC AGC TCT GGA GCC TCC CAG CTC AAT TGC CTG GGA TTT ATA CAA	450
Phe Ser Ser Ser Gly Ala Ser Gln Leu Asn Cys Leu Gly Phe Ile Gln	
105 110 115	
GAT AAA ATT ACA GTG TGT GCA ACA AAC GAC TCG TAT CAG ATG ACA CGA	498
Asp Lys Ile Thr Val Cys Ala Thr Asn Asp Ser Tyr Gln Met Thr Arg	
120 125 130 135	
GAA AGA ATG ACC CAG GCA GAG GAG GAA TCC CGC AAC CGA AGC ACA AAA	546
Glu Arg Met Thr Gln Ala Glu Glu Glu Ser Arg Asn Arg Ser Thr Lys	
140 145 150	
GTT ATC AAA CCC GGT GGA CCA TAT GTA GGG AAA AGA GTG CAA ATT CGG	594
Val Ile Lys Pro Gly Gly Pro Tyr Val Gly Lys Arg Val Gln Ile Arg	
155 160 165	
AAA GCA CCT CAA GCT GTT TCA GAT ACA GTT CCT GAG AGG AAA AGG TCA	642
Lys Ala Pro Gln Ala Val Ser Asp Thr Val Pro Glu Arg Lys Arg Ser	
170 175 180	
ACC CCC ATG AAC CCT GCA AAT ACA ATT CGA AAG ACA CAT AGC AGC AGC	690
Thr Pro Met Asn Pro Ala Asn Thr Ile Arg Lys Thr His Ser Ser Ser	
185 190 195	
ACC ATC TCT CAG AGG CCA TAC AGG GAC AGG GTG ATT CAC TTA CTG GCC	738
Thr Ile Ser Gln Arg Pro Tyr Arg Asp Arg Val Ile His Leu Leu Ala	
200 205 210 215	
CTG AAG GCC TAC AAG AAA CCG GAG CTA CTT GCT AGA CTC CAG AAA GAT	786

Leu	Lys	Ala	Tyr	Lys	Lys	Pro	Glu	Leu	Leu	Ala	Arg	Leu	Gln	Lys	Asp	
				220					225					230		
GGT	GTC	AAT	CAA	AAA	GAC	AAG	AAC	TCC	CTG	GGA	GCA	ATT	CTG	CAA	CAG	834
Gly	Val	Asn	Gln	Lys	Asp	Lys	Asn	Ser	Leu	Gly	Ala	Ile	Leu	Gln	Gln	
			235					240					245			
GTA	GCC	AAT	CTG	AAT	TCT	AAG	GAC	CTC	TCA	TAT	ACC	TTA	AAG	GAT	TAT	882
Val	Ala	Asn	Leu	Asn	Ser	Lys	Asp	Leu	Ser	Tyr	Thr	Leu	Lys	Asp	Tyr	
			250				255					260				
GTT	TTT	AAA	GAG	CTT	CAA	AGA	GAC	TGG	CCT	GGA	TAC	AGT	GAA	ATA	GAC	930
Val	Phe	Lys	Glu	Leu	Gln	Arg	Asp	Trp	Pro	Gly	Tyr	Ser	Glu	Ile	Asp	
	265					270					275					
AGA	CGG	TCA	TTG	GAG	TCA	GTG	CTC	TCT	AGA	AAA	CTA	AAT	CCG	TCT	CAG	978
Arg	Arg	Ser	Leu	Glu	Ser	Val	Leu	Ser	Arg	Lys	Leu	Asn	Pro	Ser	Gln	
280					285					290					295	
AAT	GCT	ACA	GGC	ACC	AGC	CGT	TCA	GAA	TCT	CCT	GTA	TGT	TCT	AGT	AGA	1026
Asn	Ala	Thr	Gly	Thr	Ser	Arg	Ser	Glu	Ser	Pro	Val	Cys	Ser	Ser	Arg	
				300					305					310		
GAT	GCT	GTA	TCT	TCT	CCT	CAG	AAA	CGG	CTT	TTG	GAT	TCA	GAG	TTT	ATT	1074
Asp	Ala	Val	Ser	Ser	Pro	Gln	Lys	Arg	Leu	Leu	Asp	Ser	Glu	Phe	Ile	
			315					320					325			
GAT	CCT	TTA	ATG	AAT	AAA	AAA	GCC	CGA	ATA	TCT	CAC	CTG	ACG	AAC	AGA	1122
Asp	Pro	Leu	Met	Asn	Lys	Lys	Ala	Arg	Ile	Ser	His	Leu	Thr	Asn	Arg	
			330				335						340			
GTA	CCA	CCA	ACA	CTA	AAT	GGT	CAT	TTG	AAT	CCC	ACC	AGT	GAA	AAA	TCG	1170
Val	Pro	Pro	Thr	Leu	Asn	Gly	His	Leu	Asn	Pro	Thr	Ser	Glu	Lys	Ser	
	345					350					355					
GCT	GCA	GGC	CTC	CCA	CTG	CCC	CCT	GCG	GCT	GCT	GCC	ATC	CCC	ACC	CCT	1218
Ala	Ala	Gly	Leu	Pro	Leu	Pro	Pro	Ala	Ala	Ala	Ala	Ile	Pro	Thr	Pro	
360					365				370						375	
CCA	CCG	CTG	CCT	TCA	ACC	TAT	CTG	CCC	ATC	TCA	CAT	CCT	CCT	CAG	ATT	1266
Pro	Pro	Leu	Pro	Ser	Thr	Tyr	Leu	Pro	Ile	Ser	His	Pro	Pro	Gln	Ile	
				380					385					390		
GTA	AAT	TCT	AAC	TCC	AAC	TCC	CCT	AGC	ACT	CCA	GAA	GGC	CGG	GGG	ACT	1314
Val	Asn	Ser	Asn	Ser	Asn	Ser	Pro	Ser	Thr	Pro	Glu	Gly	Arg	Gly	Thr	
			395					400					405			
CAA	GAC	CTA	CCT	GTT	GAC	AGT	TTT	AGT	CAA	AAC	GAT	AGT	ATC	TAT	GAG	1362
Gln	Asp	Leu	Pro	Val	Asp	Ser	Phe	Ser	Gln	Asn	Asp	Ser	Ile	Tyr	Glu	
			410				415						420			
GAC	CAG	CAA	GAC	AAA	TAT	ACC	TCT	AGG	ACT	TCT	CTG	GAA	ACC	TTA	CCC	1410
Asp	Gln	Gln	Asp	Lys	Tyr	Thr	Ser	Arg	Thr	Ser	Leu	Glu	Thr	Leu	Pro	
	425					430					435					
CCT	GGT	TCC	GTT	CTA	CTA	AAG	TGT	CCA	AAG	CCT	ATG	GAA	GAA	AAC	CAT	1458
Pro	Gly	Ser	Val	Leu	Leu	Lys	Cys	Pro	Lys	Pro	Met	Glu	Glu	Asn	His	
	440				445					450				455		
TCA	ATG	TCT	CAC	AAA	AAG	TCC	AAA	AAG	AAG	TCT	AAA	AAA	CAT	AAG	GAA	1506
Ser	Met	Ser	His	Lys	Lys	Ser	Lys	Lys	Lys	Ser	Lys	Lys	His	Lys	Glu	
				460				465						470		

AAG GAC CAA ATA AAA AAG CAC GAC ATT GAG ACT ATT GAG GAA AAG GAG Lys Asp Gln Ile Lys Lys His Asp Ile Glu Thr Ile Glu Glu Lys Glu 475 480 485	1554
GAA GAT CTT AAG AGA GAA GAG GAA ATT GCC AAG CTA AAT AAC TCC AGT Glu Asp Leu Lys Arg Glu Glu Glu Ile Ala Lys Leu Asn Asn Ser Ser 490 495 500	1602
CCA AAT TCC AGT GGA GGA GTT AAA GAG GAT TGC ACT GCC TCC ATG GAA Pro Asn Ser Ser Gly Gly Val Lys Glu Asp Cys Thr Ala Ser Met Glu 505 510 515	1650
CCT TCA GCA ATT GAA CTC CCA GAT TAT TTG ATA AAA TAT ATC GCT ATC Pro Ser Ala Ile Glu Leu Pro Asp Tyr Leu Ile Lys Tyr Ile Ala Ile 520 525 530 535	1698
GTC TCC TAT GAG CAA CGC CAG AAT TAT AAG GAT GAC TTC AAT GCA GAG Val Ser Tyr Glu Gln Arg Gln Asn Tyr Lys Asp Asp Phe Asn Ala Glu 540 545 550	1746
TAT GAT GAG TAC AGA GCT TTG CAT GCC AGG ATG GAG ACT GTA GCT AGA Tyr Asp Glu Tyr Arg Ala Leu His Ala Arg Met Glu Thr Val Ala Arg 555 560 565	1794
AGA TTT ATC AAA CTA GAT GCA CAA AGA AAG CGC CTT TCT CCA GGC TCA Arg Phe Ile Lys Leu Asp Ala Gln Arg Lys Arg Leu Ser Pro Gly Ser 570 575 580	1842
AAA GAG TAT CAG AAT GTT CAT GAA GAA GTC TTA CAA GAA TAT CAG AAG Lys Glu Tyr Gln Asn Val His Glu Glu Val Leu Gln Glu Tyr Gln Lys 585 590 595	1890
ATA AAG CAG TCT AGT CCC AAT TAC CAT GAA GAA AAA TAC AGA TGT GAA Ile Lys Gln Ser Ser Pro Asn Tyr His Glu Glu Lys Tyr Arg Cys Glu 600 605 610 615	1938
TAT CTT CAT AAC AAG CTG GCT CAC ATC AAA AGG CTA ATA GGT GAA TTT Tyr Leu His Asn Lys Leu Ala His Ile Lys Arg Leu Ile Gly Glu Phe 620 625 630	1986
GAC CAA CAG CAA GCA GAG TCA TGG TCC TAGAACTCTG CTTGGACCAG Asp Gln Gln Gln Ala Glu Ser Trp Ser 635 640	2033
AAGATGTGAA TAAACTTAAG CTTATTTATT TAAAATTCCA AATGAGTTGC TCTAGATTCT	2093
AAAAAGGTGA AACTTTGGCT GTTGAAAGTT TCAGTATTAG TAAACT	2139

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 640 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ala	Ala	Gly	Gly	Thr	Gly	Gly	Leu	Arg	Glu	Glu	Gln	Arg	Tyr	Gly
1				5				10						15	

Leu Ser Cys Gly Arg Leu Gly Gln Asp Asn Ile Thr Val Leu His Val
 20 25 30
 Lys Leu Thr Glu Thr Ala Ile Arg Ala Leu Glu Thr Tyr Gln Ser His
 35 40 45
 Lys Asn Leu Ile Pro Phe Arg Pro Ser Ile Gln Phe Gln Gly Leu His
 50 55 60
 Gly Leu Val Lys Ile Pro Lys Asn Asp Pro Leu Asn Glu Val His Asn
 65 70 75 80
 Phe Asn Phe Tyr Leu Ser Asn Val Gly Lys Asp Asn Pro Gln Gly Ser
 85 90 95
 Phe Asp Cys Ile Gln Gln Thr Phe Ser Ser Ser Gly Ala Ser Gln Leu
 100 105 110
 Asn Cys Leu Gly Phe Ile Gln Asp Lys Ile Thr Val Cys Ala Thr Asn
 115 120 125
 Asp Ser Tyr Gln Met Thr Arg Glu Arg Met Thr Gln Ala Glu Glu Glu
 130 135 140
 Ser Arg Asn Arg Ser Thr Lys Val Ile Lys Pro Gly Gly Pro Tyr Val
 145 150 155 160
 Gly Lys Arg Val Gln Ile Arg Lys Ala Pro Gln Ala Val Ser Asp Thr
 165 170 175
 Val Pro Glu Arg Lys Arg Ser Thr Pro Met Asn Pro Ala Asn Thr Ile
 180 185 190
 Arg Lys Thr His Ser Ser Ser Thr Ile Ser Gln Arg Pro Tyr Arg Asp
 195 200 205
 Arg Val Ile His Leu Leu Ala Leu Lys Ala Tyr Lys Lys Pro Glu Leu
 210 215 220
 Leu Ala Arg Leu Gln Lys Asp Gly Val Asn Gln Lys Asp Lys Asn Ser
 225 230 235 240
 Leu Gly Ala Ile Leu Gln Gln Val Ala Asn Leu Asn Ser Lys Asp Leu
 245 250 255
 Ser Tyr Thr Leu Lys Asp Tyr Val Phe Lys Glu Leu Gln Arg Asp Trp
 260 265 270
 Pro Gly Tyr Ser Glu Ile Asp Arg Arg Ser Leu Glu Ser Val Leu Ser
 275 280 285
 Arg Lys Leu Asn Pro Ser Gln Asn Ala Thr Gly Thr Ser Arg Ser Glu
 290 295 300
 Ser Pro Val Cys Ser Ser Arg Asp Ala Val Ser Ser Pro Gln Lys Arg
 305 310 315 320
 Leu Leu Asp Ser Glu Phe Ile Asp Pro Leu Met Asn Lys Lys Ala Arg
 325 330 335
 Ile Ser His Leu Thr Asn Arg Val Pro Pro Thr Leu Asn Gly His Leu
 340 345 350

Asn	Pro	Thr	Ser	Glu	Lys	Ser	Ala	Ala	Gly	Leu	Pro	Leu	Pro	Pro	Ala	355	360	365
Ala	Ala	Ala	Ile	Pro	Thr	Pro	Pro	Pro	Leu	Pro	Ser	Thr	Tyr	Leu	Pro	370	375	380
Ile	Ser	His	Pro	Pro	Gln	Ile	Val	Asn	Ser	Asn	Ser	Asn	Ser	Pro	Ser	385	390	395
Thr	Pro	Glu	Gly	Arg	Gly	Thr	Gln	Asp	Leu	Pro	Val	Asp	Ser	Phe	Ser	405	410	415
Gln	Asn	Asp	Ser	Ile	Tyr	Glu	Asp	Gln	Gln	Asp	Lys	Tyr	Thr	Ser	Arg	420	425	430
Thr	Ser	Leu	Glu	Thr	Leu	Pro	Pro	Gly	Ser	Val	Leu	Leu	Lys	Cys	Pro	435	440	445
Lys	Pro	Met	Glu	Glu	Asn	His	Ser	Met	Ser	His	Lys	Lys	Ser	Lys	Lys	450	455	460
Lys	Ser	Lys	Lys	His	Lys	Glu	Lys	Asp	Gln	Ile	Lys	Lys	His	Asp	Ile	465	470	475
Glu	Thr	Ile	Glu	Glu	Lys	Glu	Glu	Asp	Leu	Lys	Arg	Glu	Glu	Glu	Ile	485	490	495
Ala	Lys	Leu	Asn	Asn	Ser	Ser	Pro	Asn	Ser	Ser	Gly	Gly	Val	Lys	Glu	500	505	510
Asp	Cys	Thr	Ala	Ser	Met	Glu	Pro	Ser	Ala	Ile	Glu	Leu	Pro	Asp	Tyr	515	520	525
Leu	Ile	Lys	Tyr	Ile	Ala	Ile	Val	Ser	Tyr	Glu	Gln	Arg	Gln	Asn	Tyr	530	535	540
Lys	Asp	Asp	Phe	Asn	Ala	Glu	Tyr	Asp	Glu	Tyr	Arg	Ala	Leu	His	Ala	545	550	555
Arg	Met	Glu	Thr	Val	Ala	Arg	Arg	Phe	Ile	Lys	Leu	Asp	Ala	Gln	Arg	565	570	575
Lys	Arg	Leu	Ser	Pro	Gly	Ser	Lys	Glu	Tyr	Gln	Asn	Val	His	Glu	Glu	580	585	590
Val	Leu	Gln	Glu	Tyr	Gln	Lys	Ile	Lys	Gln	Ser	Ser	Pro	Asn	Tyr	His	595	600	605
Glu	Glu	Lys	Tyr	Arg	Cys	Glu	Tyr	Leu	His	Asn	Lys	Leu	Ala	His	Ile	610	615	620
Lys	Arg	Leu	Ile	Gly	Glu	Phe	Asp	Gln	Gln	Gln	Ala	Glu	Ser	Trp	Ser	625	630	635

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CAATTAACCC TCATAAAGGG AAC

23

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAAAGTTTCA CCTTTTAGAA TCTAGAGCAA CTC

33

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAGGTGTCGA CGAGGAGCAG CGCTATGGGC TGTCGTGCGG AC

42

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTGTGGATCC TCATCACTAG GACCATGACT CTGCTTGCTG TTG

43

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Ala	Ala	Leu	Lys	Glu	Asp	Arg	Ser	Tyr	Gly	Leu	Ser	Gly	Gly	Arg	1	5	10	15
Val	Ser	Asp	Gly	Ser	Lys	Val	Ser	Val	Phe	His	Val	Lys	Leu	Thr	Asp	20	25	30	
Ser	Ala	Ile	Arg	Ala	Phe	Glu	Ser	Tyr	Arg	Ala	Arg	Gln	Asp	Ser	Val	35	40	45	
Ser	Leu	Arg	Pro	Ser	Ile	Arg	Phe	Gln	Gly	Ser	Gln	Gly	His	Ile	Ser	50	55	60	
Ile	Pro	Gln	Pro	Asp	Cys	Pro	Ala	Glu	Ala	Arg	Thr	Phe	Ser	Phe	Tyr	65	70	75	80
Leu	Ser	Asn	Ile	Gly	Arg	Asp	Asn	Pro	Gln	Gly	Ser	Phe	Asp	Cys	Ile	85	90	95	
Gln	Gln	Tyr	Val	Ser	Ser	His	Gly	Glu	Val	His	Leu	Asp	Cys	Leu	Gly	100	105	110	
Ser	Ile	Gln	Asp	Lys	Ile	Thr	Val	Cys	Ala	Thr	Asp	Asp	Ser	Tyr	Gln	115	120	125	
Lys	Ala	Arg	Gln	Ser	Met	Ala	Gln	Ala	Glu	Glu	Glu	Ile	Arg	Ser	Arg	130	135	140	
Ser	Ala	Ile	Val	Ile	Lys	Ala	Gly	Gly	Arg	Tyr	Leu	Gly	Lys	Lys	Val	145	150	155	160
Gln	Phe	Arg	Lys	Pro	Ala	Pro	Gly	Ala	Thr	Asp	Ala	Val	Pro	Ser	Arg	165	170	175	
Lys	Arg	Ala	Thr	Pro	Ile	Asn	Leu	Ala	Ser	Ala	Ile	Arg	Lys	Ser	Gly	180	185	190	
Ala	Ser	Ala	Val	Ser	Gly	Gly	Ser	Gly	Val	Ser	Gln	Arg	Pro	Tyr	Arg	195	200	205	
Asp	Arg	Val	Ile	His	Leu	Leu	Ala	Leu	Arg	Pro	Tyr	Arg	Lys	Ala	Glu	210	215	220	
Leu	Leu	Leu	Arg	Leu	Gln	Lys	Asp	Gly	Leu	Thr	Gln	Ala	Asp	Lys	Asp	225	230	235	240
Ala	Leu	Asp	Gly	Ile	Leu	Gln	Gln	Val	Ala	Asn	Met	Ser	Ala	Lys	Asp	245	250	255	
Gly	Thr	Cys	Thr	Leu	Gln	Asp	Cys	Met	Tyr	Lys	Asp	Val	Gln	Lys	Asp				

260					265					270					
Trp	Pro	Gly	Tyr	Ser	Glu	Gly	Asp	Gln	Gln	Leu	Leu	Lys	Arg	Val	Leu
		275					280					285			
Val	Arg	Lys	Leu	Cys	Gln	Pro	Gln	Ser	Thr	Gly	Ser	Leu	Leu	Gly	Asp
	290					295					300				
Pro	Ala	Ala	Ser	Ser	Pro	Pro	Gly	Glu	Arg	Gly	Arg	Ser	Ala	Ser	Pro
305					310					315					320
Pro	Gln	Lys	Arg	Leu	Gln	Pro	Pro	Leu	Phe	Ile	Asp	Pro	Leu	Ala	Asn
				325					330					335	
Lys	Lys	Pro	Arg	Ile	Ser	His	Phe	Thr	Gln	Arg	Ala	Gln	Pro	Ala	Val
			340					345					350		
Asn	Gly	Lys	Leu	Gly	Val	Pro	Asn	Gly	Arg	Glu	Ala	Leu	Leu	Pro	Thr
		355					360					365			
Pro	Gly	Pro	Pro	Ala	Ser	Thr	Asp	Thr	Leu	Ser	Ser	Ser	Thr	His	Leu
	370					375					380				
Pro	Pro	Arg	Leu	Glu	Pro	Pro	Arg	Ala	His	Asp	Pro	Leu	Ala	Asp	Val
385					390					395					400
Ser	Asn	Asp	Leu	Gly	His	Ser	Gly	Arg	Asp	Cys	Glu	His	Gly	Glu	Ala
				405					410					415	
Ala	Ala	Pro	Ala	Pro	Thr	Val	Arg	Leu	Gly	Leu	Pro	Leu	Leu	Thr	Asp
			420					425					430		
Cys	Ala	Gln	Pro	Ser	Arg	Pro	His	Gly	Ser	Pro	Ser	Arg	Ser	Lys	Pro
		435					440					445			
Lys	Lys	Lys	Ser	Lys	Lys	His	Lys	Asp	Lys	Glu	Arg	Ala	Ala	Glu	Asp
	450					455					460				
Lys	Pro	Arg	Ala	Gln	Leu	Pro	Asp	Cys	Ala	Pro	Ala	Thr	His	Ala	Thr
465					470					475					480
Pro	Gly	Ala	Pro	Ala	Asp	Thr	Pro	Gly	Leu	Asn	Gly	Thr	Cys	Ser	Val
				485					490					495	
Ser	Ser	Val	Pro	Thr	Ser	Thr	Ser	Glu	Thr	Pro	Asp	Tyr	Leu	Leu	Lys
			500					505					510		
Tyr	Ala	Ala	Ile	Ser	Ser	Ser	Glu	Gln	Arg	Gln	Ser	Tyr	Lys	Asn	Asp
		515					520					525			
Phe	Asn	Ala	Glu	Tyr	Ser	Glu	Tyr	Arg	Asp	Leu	His	Ala	Arg	Ile	Glu
	530					535					540				
Arg	Ile	Thr	Arg	Arg	Phe	Thr	Gln	Leu	Asp	Ala	Gln	Leu	Arg	Gln	Leu
545					550					555					560
Ser	Gln	Gly	Ser	Glu	Glu	Tyr	Glu	Thr	Thr	Arg	Gly	Gln	Ile	Leu	Gln
				565					570					575	
Glu	Tyr	Arg	Lys	Ile	Lys	Lys	Thr	Asn	Thr	Asn	Tyr	Ser	Gln	Glu	Lys
			580					585					590		

His Arg Cys Glu Tyr Leu His Ser Lys Leu Ala His Ile Lys Arg Leu
595 600 605

Ile Ala Glu Tyr Asp Gln Arg Gln Leu Gln Ala Trp Pro
610 615 620

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Asp Trp Ile Arg Glu Tyr Pro Pro Ile Thr Ser Asp Gln Gln Arg Gln
1 5 10 15
Leu Tyr Lys Arg Asn Phe Asp Thr Gly Leu Gln Glu Tyr Lys Ser Leu
20 25 30
Gln Ser Glu Leu Asp Glu Ile Asn Lys Glu Leu Ser Arg Leu Asp Lys
35 40 45
Glu Leu Asp Asp Tyr Arg Glu Glu Ser Glu Glu Tyr Met Ala Ala Ala
50 55 60
Asp Glu Tyr Asn Arg Leu Lys Gln Val Lys Gly Ser Ala Asp Tyr Lys
65 70 75 80
Ser Lys Lys Asn His Cys Lys Gln Leu Lys Ser Lys Leu Ser His Ile
85 90 95
Lys Lys Met Val Gly Asp Tyr Asp Arg Gln Lys Thr
100 105

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTCCACCGCT GCCTTCAACC TATCTGCCCA TCTCACATCC TCCTCAGATT GTAAATTCTA 60
ACTCCAACCTC CCCTAGCACT CCAGAAGGCC GGGGGACTCA AGACCTACCT GTTGACAGTT 120

TTAGTCAAAA CGATAGTATC TATGAGGACC AGCAAGACAA ATATACCTCT AGGACTTCTC	180
TGGAAACCTT ACCCCCTGGT TCCGTTCTAC TAAAGTGTCC AAAGCCTATG GAAGAAAACC	240
ATTCATGTG TCACAAAAAG TCCAAAAAGA AGTCTAAAAA ACATAAGGAA AAGGACC	297

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 358 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGCAACCGAA GCACAAAAGT TATCAAACCC GGTGGACCAT ATGTAGGGAA AAGAGTGCAA	60
ATTCGGAAG CACCTCAAGC TGTTTCAGAT ACAGTTCCTG AGAGGAAAAG GTCAACCCCC	120
ATGAACCCTG CAAATACAAT TCGAAAGACA CATAGCAGCA GCACCATCTC TCAGAGGCCA	180
TACAGGGACA GGGTGATTCA NTTACTGGCC CTGAAGGCCT ACAAGAAACC GGAGCTACTT	240
GCTAGACTCC AGAAAGATGG TGTCAATCAA AAAGACAAGA ACTCCCTGGG GAGGCAATTN	300
TTGCAACAGG TAGNCCAATC TGGATTCTA AGGGACCTCT TCATATTACC TTAAAGG	358

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 362 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGCGNCGTNN TCGNCGGGCA CCCCAGGGGAG TTTGAAGATG GCGGCGGGGG GGACAGGGGG	60
CCTNCGGGAG GAGCAGCGCT ATGGGCTGTC GTGCCGGACG GCTGGGGCAG GACAACATCA	120
CCGTACTGCA TGTNAAAGCT TCACCGAGAC GGNCGATTCC GGGGCGGTTC GAGAACTTAC	180
CAGAGCCACA AGNNTTTNAA TTCCCTTTTC GGACCTTCAA TCCAGTTTCC AAGGACTCCA	240
CGGGCTTTGT NCAAAAATTT CCCAAAAATG ATTCCCCTTC AATGGANAGT TCATAAATTT	300
TAAATTTTAA ATTTGTTCAA ATNTGGGGN AAAGNCAAAC CTTCAAGGGC NAGTTTTGGA	360
CT	362

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 477 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AATTCGGCAC GAGCATGGTC CTAGAACTCT GCTTNGACCA GAAGATGTGA ATAAACTTAA	60
GCTTATTTAT TTAAAATTCC AAATGAGTTN NTCTAGNTTC TAAAAAGGTG AAACTTTGGC	120
TGTTGAAAGT TTCAGTATTA GTAAACTTGA GTTACTTTNN CTTTTCCATT TNACTTTGCT	180
TCCCTGCATT TCGAAGCTGC TCTTCTGGT CCTCCCCACC ACCCCACCCC CAAGACTTGT	240
GTTTGTTAAT AGAAATAATT TTTTtagGTA TTGGGGATCC ATTGTCTATT ATTTCAAATC	300
AAGNTTTTTN TTTNTCCTCA AAAANCTTGT GGTTTTGTGA TTAGGAAATG GNTTTTTTAG	360
ATATTGGGGN TCCAGTGTCC NACTTGAAA AGGTGGGNAG GGGTTTAAAA AANAGCANCA	420
GTAATNTGCA AGGTGNAATG NTTTTGGTNA ACGGANGCCA TTTTCCGACG TNCTTAA	477

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 178 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AAACATTCTC CAGCTCTGGG ACCTCCCAN C TCAATTCCTT GGAATTNAT ACAAGATAAA	60
ATTACAGTGT GTGCACAAAC GACTCGTATC AAATGACACG AGAAANANTG ACCCAGGCAG	120
NGGAGGGAAT CCCGCAACCA ANGACAAAA GTTATTCAAA CCCGGTGGGA CCATATNT	178

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 158 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GNCCTTTCTC CANTCTCAAA AGNGNTATCA CAATGTTTCAT GNAAGAAGTC TTACAAGAAT	60
ATCAGAAGAT AAAGCCAGTC TAGTCCCAAT TACCATGAAG NAAAAATACA GATGTGNAAT	120
ATCTTCATAA CAAGCTGGCT CACATCAAAA GGCTAATN	158

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATAAATAAGC TTAAGTTTAT TCACATCTTC TGGTCCAAGC AGAGTTCTAG GACCATGACT	60
CTGCTTGCTG TTGGTCAAAT TCACCTATTA GCCTTTTGAT GTGAGCCAGC TTGTTATGAA	120
GATATTCACA TCTGTATTTT TCTTCATGGT AATTGGGACT AGACTGCTTT ATCTTCTGAT	180
ATTCTTGTA A GACTTCTTCA TGAACATTCT GATACTCTTT TGAGCCTGGA GAAAGGCGCT	240
TTCTTTGTGC ATCTAGTTTG ATAAATCTTC TAGCTACAGT CTCCATCCTG GCATGCAAAG	300
CTCTGTACTC ATCATACTCT GCATTGAAGT CATCCTTATA ATTCTGGCGT TGCTCATAGG	360
AGACGATAGC GATATATTTT ATCAAATAAT CTGGGAGTTC AATTGCTGAA GGGTCCATGG	420
AGGCAGTGCA ATCCTCTT	438

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGCNCCGCAG TGGANGGCTA GAGCGNAGCG CGCGGCGGCG GNCACCCCGG GGAGTTTAAG	60
ATGGCGGCNG GGGGGACAGG GGGCCTGCGG GAGGAGCAGC GCTATGGGCT GTCGTGCGGA	120
CGGCTGGGGC AGGACAACAT CACCGTACTG CATGTGAAGC TCACCGAGAC GGCGATCCGG	180

GCGCTCGAGA CTTACCAGAG CCACAAGAAT TTAATTCCTT TTCGACCTTC AATCCAGTTC 240
CAAGGACTCC ACGGGCTTGT CAAAATTCCC AAAAATGATC CCCTCAATGA AGTTCATAAC 300
TTTAACTTTT ATTTGTCAAA TGTGGGCAAA GACAACCCTC AGGGCAAGCT TTGACTGCAT 360
CCAGCAAACA TTCTCCAGCT CTGGAGCCTC CCAGCTCAAT TGCCTNNGGA TTTATACAAG 420
ATAAAATTAC AGTGTGTGCA ACAAACGACT CGTATCAGA 459

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 412 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TGGGATTCAA ATGACCATTT AGTGTGGTG GTACTCTGTT CGTCAGGTGA GATATTCGGG 60
CTTTTTTATT CATTAAAGGA TCAATAAACT CTGAATCCAA AAGCCGTTTC TGAGGAGAAG 120
ATACAGCATC TCTACTAGAA CATAACAGGAG ATTCTGAACG GCTGGTGCCT GTAGCATTCT 180
GAGACGGATT TAGTTTTCTA GAGAGCACTG ACTCCAATGA CCGTCTGTCT ATTTCACTGT 240
ATCCAGGCCA GTCTCTTTGA AGCTCTTTAA AACATAATC CTTTAAGGGA TATGAGAGGT 300
CCTTAGAATT CAGATTGGCT AGCTGTTGCA GAATTGCTCC CAGGGAGTTC TTGTCTTTTT 360
GATTGACACC ATCTTTCTGG AGTCCTACAA GTAGCTCCGG GTTTCTTGTA GG 412

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 487 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCAAATAAAG AAAGTTGACA TTGAGACCAT GGAGGAGAAG GAGGAAGACC TTCAGAGAGA 60
AGAAACTGCC AAGCTGAGTA ATGCCAGTCC AAATCCCAAT GAAGGAGTTA AAGAAGGGTG 120
CACAGCCTCC ATGGAGCCTT CTTGAGCACT TGAAGTCCCA GATTATTTGA TAAATATAT 180
TGCTATTGTC TCTTATGAGC AACGCCAGAA TTACAAGGAT GACTTCAATG CTGAGTATGA 240

TGAATACAGA GCTTTGCATG CAAGGATGGA GACTGTAGCC AGGAGATTTA TTAAACTGGA	300
TGCACAACGA AAACGCCTTT CTCCAGGTTT AAAAGAGTAC CAGAATGTTT ATGAAGAAGT	360
CTTACAGGAA TATCAGAAGA TCAAGCAGTC CAGTCCCAAT TACCATGAAG AAAAATACAG	420
ATGTGAATAT CTTCATAACA AGCTGGCTCA CATCAAAGAC TAATAGGTCG AATTTGACCA	480
ACAGCAA	487

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 525 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GCTTTGCATG CCAGGATGGA GACTGTAGCT AGAAGATTTA TCAAACCTAGA TGCACAAAGA	60
AAGCGCCTTT CTCCAGGCTC AAAAGAGTAT CAGAATGTTT ATGAAGAAGT CTTACAAGAA	120
TATCAGAAGA TAAAGCAGTC TAGTCCCAAT TACCATGAAG AAAAATACAG ATGTGAATAT	180
CTTCATAACA AGCTGGCTCA CATCAAAGG CTAATAGGTG AATTTGACCA ACAGCAAGCA	240
GAGTCATGGT CCTAGAACTC TGCTTGACC AGAAGATGTG AATAAACTTA AGCTTATTTA	300
TTTAAAATTC CAAATGAGTT GCTCTAGATT CTAAAAGGT GAAACTTTGG CTGTTGAAAG	360
TTTCAGTATT AGTAAACTTN GAGTTACTTT TTCTTTTCCA TTTTACTTTG CTTCCCTGCA	420
TTTCGGAAGC TGCCTCTTTN CTGGGTCCTC NCCACTNGGG GCCAGCCCCC AAGNACTTGG	480
TGTTTTGGTT AATAGGNAAT AATTTTCTTT AAGGGAATTG GGGGA	525

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 455 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TTAGTCAAAA TGGTAGCATC TTTGAGGACC AGCAAGAAAA ATATACCTCA AGGACTTGTC	60
TGGAAACATT ACCCCCCAGC TCAGCTCTGC TAAAGTGTCC AAAGCCCATG GAAGAAGAGC	120

ATCCAGTGTC TCACAAAAAG TCCAAAAAGA AGTCTAAAAA ACACAAGGAA AAGGACCAAA	180
TAAAGAACT TGACATTGAG ACCATGGAGG AGAAGGAGGA AGACCTTCAG AGAGAAGAAA	240
CTGCCAAGCT GAGTAATGCC AGTCCAAATC CCAATGAAGG AGTTAAAGAA GGGTGCACAG	300
CCTCCATGGA GCCTTCTTCA GCACTTGAAC TCCCAGATTA TTTGATAAAA TATATTGCTA	360
TTGTCTCTTA TGAGCAACGC CAGAATTACA AGGATGACTT CAATGCTGAG TATGATGAAT	420
ACAGAGCTTT GCATGCAAGG ATGGAGACTG TAGCG	455

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TCACCTACTG GCCCTGAAGG CTACAAGAAA CCGGAGCTAC TTGCTAGACT CCAGAAAGAT	60
GGTGTCAATC AAAAAGACAA GAACTCCCTG GGAGCAATTC TGCAACAGGT AGCCAATCTG	120
AATTCTAAGG ACCTCTCATA TACCTTAAAG GATTATGTTT TTAAAGAGCT TCAAAGAGAC	180
TGGCCTGGNT ACAGTGAAAT AGACAGACGG TCATTGGAGT CAGTGCTCTC TAGAAACTA	240
AATCCGTCTC AGAATGCTAC AGGCACCAGC CTNTCAGAAT CTCCTGTATG TTCTAGTAGA	300
GATGCTGTAT CTTCTCCTCA GGAAACGGCT TTTGGGTTTC AGAGTTTATT TGATCCCTTT	360
AATGGANTTA AAAAAGGCT	379

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

NTCACTTACT GGCCCTGAAG CTANCAAGAA ACCGGAGCTA CTGCTAGAC TCCAGAAAGA	60
TGGTGTCAAT CAAAAGACA AGAACTCCCT GGGAGCAATT CTGCAACAGG TAGCCAATCT	120
GAATTCTAAG GACCTCTCAT ATACCTTAAA GGATTATGTT TTAAAGAGC TTCAAAGAGA	180

CTGGCCTGGG ATACAGTGAA ATAGACAGAC GGTCATTGGA GTCAGTGCTC TCTAGAAAAC 240
TAAATCCGTC TCAGAATGCT ACAGGCACCA GCGTTTCAGA ATCTCCTGTA TGTTC TAGTA 300
GGAGATGCTG TATCTTCTCC TCAGGAAACG GCTTTTGGGT TCAGGAGTTT ATTTGATCCN 360
TTTAATGGAT TAAAAAAGGC CCCGATTATT CTTCACCTGG ACGGAACAGA GTTACCNCCC 420
AACATTAATG GGTCCNTTTG GATTCCCACC AGTGGAAAAT TGGGTGGCGG GCTTNCCCAT 480
TGCCCCTGNG GGTGGTGGCN TTCCCCACCC TTNCACCGG 519

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CTCCACCGCT GCCTTCAACC TATCTGCCCA TCTCACATCC TCCTCAGATT GTAAATTCTA 60
ACTCCAATC CCCTAGCACT CCAGAAGGCC GGGGGACTCA AGACCTACCT GTTGACAGTT 120
TTAGTCAAAA CGATAGTATC TATGAGGACC AGCAAGACAA ATATACCTCT AGGACTTCTC 180
TGGAACCTT ACCCCCTGGT TCCGTTCTAC TAAAGTGTC AAAGCCTATG GAAGAAAACC 240
ATTCAATGTC TCACAAAAAG TCAAAAAAGA AGTCTAAAAA ACATAAGGAA AAGGACC 297

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CGCAACCGAA GCACAAAAGT TATCAAACCC GGTGGACCAT ATGTAGGGAA AAGAGTGCAA 60
ATTCGGAAAG CACCTCAAGC TGTTCAGAT ACAGTTCCTG AGAGGAAAAG GTCAACCCCC 120
ATGAACCCTG CAAATACAAT TCGAAAGACA CATAGCAGCA GCACCATCTC TCAGAGGCCA 180
TACAGGGACA GGGTGATTCA NTTACTGGCC CTGAAGGCCT ACAAGAAACC GGAGCTACTT 240
GCTAGACTCC AGAAAGATGG TGTCAATCAA AAAGACAAGA ACTCCCTGGG GAGGCAATTN 300

TTGCAACAGG TAGNCCAATC TGGATTCTTA AGGGACCTCT TCATATTACC TTAAAGG

358

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 285 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TTTTGTGAGA CATTGAATGG TTTTCTTCCA TAGGCTTTGG ACACCTTAGT AGAACGGAAC	60
CAGGGGGTAA GGTTTCCAGA GAAGTCCTAG AGGTATATTT GTCTTGCTGG TCCTCATAGA	120
TACTATCGTT TTGACTAAAA CTNTCAACAG GTAGGTCTTG AGTCCCCCGG CCTTCTGGAG	180
TGCTAGGGGA GTTGAGTTA GAATTTACAA TCTGAGGAGG ATGTGAGATG GGCAGATAGG	240
TTGAAGGCAG CGGTGGAGGG GTGGGGATGG CAGCAGCCCA GGGGG	285

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 431 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TTTATTCCAA ACAGCATCAT CTACAACCTA TAATCGCAGG CTCCTCCAGT TCATTTAACA	60
CAGAAAGCAG GCTTTTTTCT CTTTTCCCAT TTAAACAAAT GTAAAATACC TTCATTGGGA	120
TTTGGACTGG CATTACTCAG CTTGGCAGTT TCTTCTCTCT GAAGGTCTTC CTCCTTCTCC	180
TCCATGGTCT CAATGTCAAG TTTCTTTATT TGGTCCTTTT CTTGTGTTT TTTAGACTTC	240
TTTTTGGACT TTTTGTGAGA CACTGGATGC TCTTCTTCCA TGGGCTTTGG ACACCTTAGC	300
AGAGTGAGCT GGGGGGTAAAT GTTTCCAGAC AAGTCCTTGA GGTATATTTT TCTTGCTGGT	360
CCTCAAAGAT GCTACCATTT TGACTAAAAC TGTCACAGG CAGGTCTTGA GTCCAGGCC	420
TTCTGGAGTG C	431

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 196 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```
CACCGAGACG GCGATCCGGG CGCTCGAGAC TTACCAGAGC CACAAGAATT TAATTCCTTT      60
TCGACCTTCA ATCCAGTTCC AAGGACTCCA CGGGCTTGTC AAAATTCCCA AAAATGATCC      120
CCTCAATGAA GTTCATAACT TTAACITTTA TTTGTCAAAT GTGGGCAAAG ACAACCCTCA      180
GGGGAGCTTG GGCTGC                                          196
```

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 197 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```
ACCATCTCTC AGAGGCCATA CAGGGACAGG GTGATTCACT TACTGGCCCT GAAGGCNTAC      60
AAGAAACCGG AGCTACTTGC TAGACTCCAG AAAGATGGTG TCAATCAAAA AGACAAGAAC      120
TCCCTGGGAG CAATTCTGCA ACAGGTAGCC AATCTGAATN CTAAGGACCT CNTCATATAC      180
CTTAAAGGAT TATGTTT                                          197
```

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 348 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```
GCGCCCGGCA GTGGAGGCTA GAGCCGACG GCGCGGCGGG CGGACACCGC CGGGGAGGTT      60
TAAGAGTGGC GGCTGGGGGG GACAGGGGGG CCTGCAGGGA GGAGCAGCGC TATGGGCTGT      120
CGTGCGGACG GCGTGGGGCA GGACAACATC ACCGTACTGC ATGTGAAGCT CACCGAGACG      180
```

GCGATCCGGG CGCTCGAGAC TTACCAGAGC CACAAGAATT TAATTCCTTT TCGACCTTCA 240
ATCCAGTTCC AAGGACTCCA CGGGGTGAGT ACTCTTATTG ATTTAACAAA CAAATCTAAT 300
GTTCTTGCAC GCTATTCAAC TTTTAAATC CGTTTTTCAGT TGACCCTT 348

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 184 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GGAATTTTAA ATAAATAAGC TTAAGTTTAT TCACATCTNC TGGTCCAAGC AGAGTTCTAG 60
GACCATGACT CTGCTTGCTG TTGGTCAAAT TCACCTATTA GCCTTTNGAT GTGAGCCAGC 120
TTGTTATGAA GATATTCACA TCTGTATTTT NCTTCATGGT AATTGGGACT AGACTGCTTT 180
ATCT 184

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 280 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TCCTAGAACT CTGCTTGGAC CAGAAGATGT GAATAAACTT AAGCTTATTT ATTTAAAATC 60
ACAAATGAGT TGCTCTAGAT TCTAAAAGGG TGAAACTTTG ACTGTTGAAA GTTTAAGTAT 120
TAGTAACTT GAGTTACTTT TTCTTTCAAA TTTCACTCCG CTTCCCTGCA TTTCGAAGCT 180
GCTCTTCTG GTCCTACCCA CCACCCACC AACAAGACTT GTGTTTGTTA ATAGAAATAA 240
TTTATCAAGG TATTGGGGAT CCATTGTCTA TATTTAAAC 280

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 255 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

AACTAGCAGT CCCTTTGGGC CAATTGATGT AATTATTTTC AGTGTAATC CNAAAGGTTG	60
CCTGTTTTAN GNTAGGAGAT GATAGTAAAA ATACCTAATG CTCTGTTTTT ATACCTCATA	120
CTAGGTAGCC AATCTGAATT CTAAGGACCT CTCATATACC TTAAAGGATT ATGTTTNTAA	180
AGAGCTTCAA AGAGACTGGC CTGGATACAG TGAAATAGAC AGACGGTCAT TGGAGTCATG	240
TGCTCTCTAG GTGAA	255

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3974 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GGTACCTAAG TGAGTAGGGC GTCCGATCGA CGGACGCCCTT TTTTTGAAT TCGTAATCAT	60
GGTCATAGCT GTTTCCTGTG TGAAATTGTT ATCCGCTCAC AATCCACAC AACATACGAG	120
CCGGAAGCAT AAAGTGTAAG GCCTGGGGTG CCTAATGAGT GAGCTAACTC ACATTAATTG	180
CGTTGCGCTC ACTGCCCCGCT TTCCAGTCGG GAAACCTGTC GTGCCAGCTG CATTAATGAA	240
TCGGCCAACG CGCGGGGAGA GGCGGTTTGC GTATTGGGCG CTCTTCCGCT TCCTCGCTCA	300
CTGACTCGCT GCGCTCGGTC GTTCGGCTGC GCGGAGCGGT ATCAGCTCAC TCAAAGGCGG	360
TAATACGGTT ATCCACAGAA TCAGGGGATA ACGCAGGAAA GAACATGTGA GCAAAAGGCC	420
AGCAAAAGGC CAGGAACCGT AAAAAGGCCG CGTTGCTGGC GTTTTTCCAT AGGCTCCGCC	480
CCCCTGACGA GCATCAGAAA AATCGACGCT CAAGTCAGAG GTGGCGAAAC CCGACAGGAC	540
TATAAAGATA CCAGGCGTTT CCCCTGGAA GCTCCCTCGT GCGCTCTCCT GTTCCGACCC	600
TGCCGCTTAC CGGATACCTG TCCGCCTTTC TCCCTTCGGG AAGCGTGGCG CTTTCTCATA	660
GCTCACGCTG TAGGTATCTC AGTTCGGTGT AGGTCGTTTC CTCCAAGCTG GGCTGTGTGC	720
ACGAACCCCC CGTTCAGCCC GACCGCTGCG CTTATCCGG TAACTATCGT CTTGAGTCCA	780
ACCCGGTAAG ACACGACTTA TCGCCACTGG CAGCAGCCAC TGGAACAGG ATTAGCAGAG	840
CGAGGTATGT AGGCGGTGCT ACAGAGTTCT TGAAGTGGTG GCCTAACTAC GGCTACACTA	900

GAAGAACAGT	ATTTGGTATC	TGCGCTCTGC	TGAAGCCAGT	TACCTTCGGA	AAAAGAGTTG	960
GTAGCTCTTG	ATCCGGCAAA	CAAACCACCG	CTGGTAGCGG	TGGTTTTTTT	GTTTGCAAGC	1020
AGCAGATTAC	GCGCAGAAAA	AAAGGATCTC	AAGAAGATCC	TTTGATCTTT	TCTACGGGGT	1080
CTGACGCTCA	GTGGAACGAA	AACTCACGTT	AAGGGATTTT	GGTCATGAGA	TTATCGTCGA	1140
CAATTCGCGC	GCGAAGGCGA	AGCGGCATGC	ATTTACGTTG	ACACCATCGA	ATGGTGCAAA	1200
ACCTTTCGCG	GTATGGCATG	ATAGCGCCCG	GAAGAGAGTC	AATTCAGGGT	GGTGAATGTG	1260
AAACCAGTAA	CGTTATACGA	TGTCGCAGAG	TATGCCGGTG	TCTCTTATCA	GACCGTTTCC	1320
CGCGTGGTGA	ACCAGGCCAG	CCACGTTTCT	GCGAAAACGC	GGGAAAAAGT	GGAAGCGGCG	1380
ATGGCGGAGC	TGAATTACAT	TCCCAACCGC	GTGGCACAAC	AACTGGCGGG	CAAACAGTCG	1440
TTGCTGATTG	GCGTTGCCAC	CTCCAGTCTG	GCCCTGCACG	CGCCGTCGCA	AATTGTCGCG	1500
GCGATTAAAT	CTCGCGCCGA	TCAACTGGGT	GCCAGCGTGG	TGGTGTCGAT	GGTAGAACGA	1560
AGCGGCGTCG	AAGCCTGTAA	AGCGGCGGTG	CACAATCTTC	TCGCGCAACG	CGTCAGTGGG	1620
CTGATCATTA	ACTATCCGCT	GGATGACCAG	GATGCCATTG	CTGTGGAAGC	TGCCTGCACT	1680
AATGTTCCGG	CGTTATTTCT	TGATGTCTCT	GACCAGACAC	CCATCAACAG	TATTATTTTC	1740
TCCCATGAAG	ACGGTACGCG	ACTGGGCGTG	GAGCATCTGG	TCGCATTGGG	TCACCAGCAA	1800
ATCGCGCTGT	TAGCGGGCCC	ATTAAGTTCT	GTCTCGGCGC	GTCTGCGTCT	GGCTGGCTGG	1860
CATAAATATC	TCACTCGCAA	TCAAATTCAG	CCGATAGCGG	AACGGGAAGG	CGACTGGAGT	1920
GCCATGTCCG	GTTTTCAACA	AACCATGCAA	ATGCTGAATG	AGGGCATCGT	TCCCACTGCG	1980
ATGCTGGTTG	CCAACGATCA	GATGGCGCTG	GGCGCAATGC	GCGCCATTAC	CGAGTCCGGG	2040
CTGCGCGTTG	GTGCGGATAT	CTCGGTAGTG	GGATACGACG	ATACCGAAGA	CAGCTCATGT	2100
TATATCCCGC	CGTTAACCAC	CATCAAACAG	GATTTTCGCC	TGCTGGGGCA	AACCAGCGTG	2160
GACCGCTTGC	TGCAACTCTC	TCAGGGCCAG	GCGGTGAAGG	GCAATCAGCT	GTTGCCCCGC	2220
TCACTGGTGA	AAAGAAAAAC	CACCCTGGCG	CCCAATACGC	AAACCGCCTC	TCCCCGCGCG	2280
TTGGCCGATT	CATTAATGCA	GCTGGCACGA	CAGGTTTCCC	GACTGGAAAG	CGGGCAGTGA	2340
GCGCAACGCA	ATTAATGTAA	GTTAGCGCGA	ATTGTCGACC	AAAGCGGCCA	TCGTGCCTCC	2400
CCACTCCTGC	AGTTCGGGGG	CATGGATGCG	CGGATAGCCG	CTGCTGGTTT	CCTGGATGCC	2460
GACGGATTTG	CACTGCCGGT	AGAACTCCGC	GAGGTCGTCC	AGCCTCAGGC	AGCAGCTGAA	2520
CCAACCTCGC	AGGGGATCGA	GCCCCGGGTG	GGCGAAGAAC	TCCAGCATGA	GATCCCCGCG	2580
CTGGAGGATC	ATCCAGCCGG	CGTCCCGGAA	AACGATTCCG	AAGCCCAACC	TTTCATAGAA	2640
GGCGGCGGTG	GAATCGAAAT	CTCGTGATGG	CAGGTTGGGC	GTCGCTTGGT	CGGTCAATTC	2700
GAACCCAGAG	GTCCCGCTCA	GAAGAACTCG	TCAAGAAGGC	GATAGAAGGC	GATGCGCTGC	2760

GAATCGGGAG CGGCGATACC GTAAAGCACG AGGAAGCGGT CAGCCCATTTC GCCGCCAAGC	2820
TCTTCAGCAA TATCACGGGT AGCCAACGCT ATGTCCTGAT AGCGGTCCGC CACACCCAGC	2880
CGGCCACAGT CGATGAATCC AGAAAAGCGG CCATTTTCCA CCATGATATT CGGCAAGCAG	2940
GCATCGCCAT GGGTCACGAC GAGATCCTCG CCGTCGGGCA TGC GCGCCTT GAGCCTGGCG	3000
AACAGTTCGG CTGGCGCGAG CCCCTGATGC TCTTCGTCCA GATCATCCTG ATCGACAAGA	3060
CCGGCTTCCA TCCGAGTACG TGCTCGCTCG ATGCGATGTT TCGCTTGGTG GTCGAATGGG	3120
CAGGTAGCCG GATCAAGCGT ATGCAGCCGC CGCATTG CAT CAGCCATGAT GGATACTTTC	3180
TCGGCAGGAG CAAGGTGAGA TGACAGGAGA TCCTGCCCCG GCACTTCGCC CAATAGCAGC	3240
CAGTCCCTTC CCGCTTCAGT GACAACGTCG AGCACAGCTG CGCAAGGAAC GCCCGTCGTG	3300
GCCAGCCACG ATAGCCGCGC TGCCTCGTCC TGCAGTTCAT TCAGGGCACC GGACAGGTCG	3360
GTCTTGACAA AAAGAACCGG GCGCCCCTGC GCTGACAGCC GGAACACGGC GGCATCAGAG	3420
CAGCCGATTG TCTGTTGTGC CCAGTCATAG CCGAATAGCC TCTCCACCCA AGCGGCCGGA	3480
GAACCTGCGT GCAATCCATC TTGTTCAATC ATGCGAAACG ATCCTCATCC TGTCTCTTGA	3540
TCAGATCTTG ATCCCCTGCG CCATCAGATC CTTGGCGGCA AGAAAGCCAT CCAGTTTACT	3600
TTGCAGGGCT TCCCAACCTT ACCAGAGGGC GCCCAGCTG GCAATTCCGG TTCGCTTGCT	3660
GTCCATAAAA CCGCCCAGTC TAGCTATCGC CATGTAAGCC CACTGCAAGC TACCTGCTTT	3720
CTCTTTGCGC TTGCGTTTTT CTTGTCCAG ATAGCCCAGT AGCTGACATT CATCCGGGGT	3780
CAGCACCGTT TCTGCGGACT GGCTTTCTAC GTGTTCCGCT TCCTTTAGCA GCCCTTGCGC	3840
CCTGAGTGCT TGCGGCAGCG TGAAGCTTAA AAAACTGCAA AAAATAGTTT GACTTGTGAG	3900
CGGATAACAA TTAAGATGTA CCCAATTGTG AGCGGATAAC AATTTCACAC ATTAAAGAGG	3960
AGAAATTACA TATG	3974

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 112 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

AAGCTTAAAA AACTGCAAAA AATAGTTTGA CTTGTGAGCG GATAACAATT AAGATGTACC	60
CAATTGTGAG CGGATAACAA TTTCACACAT TAAAGAGGAG AAATTACATA TG	112